Online-Only Abstract

Extrapulmonary infections caused by a dominant strain of *Mycobacterium massiliense* (*Mycobacterium abscessus subspecies bolletii*)

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Abstract

A single strain of *Mycobacterium massiliense* (BRA 100), a subspecies of the *Mycobacterium abscessus* complex, has been responsible for an epidemic of post-surgical infections in Brazil. Outside Brazil, this is the first report to describe a single emerging strain of *M. massiliense* (TPE 101) associated with extrapulmonary infections. This phenomenon may be underestimated because sophisticated molecular typing of *M. abscessus* is not routinely performed. Our molecular epidemiology study was triggered by an outbreak investigation. Nine case isolates were grown from the surgical sites of nine mostly paediatric patients receiving operations from 2010 to 2011. All available non-duplicated isolates of *M. abscessus* during this period were obtained for comparison. Mycobacteria were characterized by multilocus sequence analysis (MLSA), repetitive sequence PCR (rep-PCR) and pulsed-field gel electrophoresis (PFGE). Of 58 isolates of *M. abscessus* overall, 56 were clinical isolates. MLSA identified 36 of the isolates as *M. massiliense*. All case isolates were indistinguishable by PFGE and named the TPE 101 pulsotype. Of the stored strains of *M. abscessus*, TPE 101 strains were over-represented among the control surgical wound (7/7, 100%) and subcutaneous tissue isolates (4/5, 80%) but rare among the respiratory isolates (1/16, 6%) and absent from external skin, ocular and environmental samples. In conclusion, a unique strain of *M. massiliense* has emerged as a distinctive pathogen causing soft tissue infections in Taiwan. Further study to identify whether this is due to an occult common source or to specific virulence factors dictating tissue tropism is warranted.